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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/331,631A DATE: 12/28/2000
TIME: 08:00:58

Input Set : A:\CULLN23SEQ.txt
Output Set: N:\CRF3\12282000\I331631A.raw

4 <110> APPLICANT: Manners, John M.
5 Marcus, John Paul
6 Goulier, Kenneth C.
7 Green, Jodie L.
9 <120> TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
12 <130> FILE REFERENCE: CULLN23.001APC
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/331,631A
C--> 14 <141> CURRENT FILING DATE: 1999-06-21
14 <150> PRIOR APPLICATION NUMBER: PCT/AU97/00874
15 <151> PRIOR FILING DATE: 1997-12-22
17 <150> PRIOR APPLICATION NUMBER: AU PO 4275
18 <151> PRIOR FILING DATE: 1996-12-20
20 <160> NUMBER OF SEQ ID NOS: 40
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 666
26 <212> TYPE: PRT
27 <213> ORGANISM: Macadamia integrifolia
29 <400> SEQUENCE: 1
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31 1 5 10 15
32 Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
33 20 25 30
34 Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Glu Leu Glu Thr
35 35 40 45
36 Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
37 50 55 60
38 Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Glu Asp Pro Gln Thr
39 65 70 75 80
40 Glu Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro
41 85 90 95
42 Arg Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu
43 100 105 110
44 Glu Glu Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Gln Tyr Glu Gln
45 115 120 125
46 Cys Gln Lys His Cys Gln Arg Arg Glu Thr Glu Pro Arg His Met Gln
47 130 135 140
48 Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys
49 145 150 155 160
50 Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr
51 165 170 175
52 Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg
53 180 185 190
54 Glu Tyr Glu Asp Cys Arg Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln
55 195 200 205
56 Gln His Gln Cys Gln Leu Arg Cys Arg Glu Gln Gln Arg Gln His Gly
57 210 215 220

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58 Arg Gly Gly Asp Met Met Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
 59 225 230 235 240
 60 Glu Glu Gly Glu Glu Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
 61 245 250 255
 62 Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
 63 260 265 270
 64 Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
 65 275 280 285
 66 Tyr Arg Leu Val Leu Leu Ala Asn Pro Asn Ala Phe Val Leu Pro
 67 290 295 300
 68 Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Ile Gly Gly Arg Gly
 69 305 310 315 320
 70 Ala Leu Lys Met Ile His His Asp Asn Arg Glu Ser Tyr Asn Leu Glu
 71 325 330 335
 72 Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
 73 340 345 350
 74 Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
 75 355 360 365
 76 Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
 77 370 375 380
 78 Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
 79 385 390 395 400
 80 Ala Leu Asn Thr Gln Thr Glu Lys Leu Arg Gly Val Phe Gly Gln Gln
 81 405 410 415
 82 Arg Glu Gly Val Ile Ile Arg Ala Ser Gln Glu Gln Ile Arg Gln Leu
 83 420 425 430
 84 Thr Arg Asp Asp Ser Glu Ser Arg His Trp His Ile Arg Arg Gly Gly
 85 435 440 445
 86 Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
 87 450 455 460
 88 Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
 89 465 470 475 480
 90 Gln Leu Gln Asp Met Asp Leu Ser Val Phe Ile Ala Asn Val Thr Gln
 91 485 490 495
 92 Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
 93 500 505 510
 94 Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu
 95 515 520 525
 96 Ser Gly Arg His Gly Gly Arg Gly Gly Lys Arg His Glu Glu Glu
 97 530 535 540
 98 Glu Asp Val His Tyr Glu Glu Val Arg Ala Arg Leu Ser Lys Arg Glu
 99 545 550 555 560
 100 Ala Ile Val Val Leu Ala Gly His Pro Val Val Phe Val Ser Ser Gly
 101 565 570 575
 102 Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
 103 580 585 590
 104 His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
 105 595 600 605
 106 Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val

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Input Set : A:\CULLN23SEQ.txt
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107 610 615 620
108 Glu Glu Ser Phe Asn Ser Gln Asp Gln Ser Ile Phe Phe Pro Gly Pro
109 625 630 635 640
110 Arg Gln His Cln Gln Ser Pro Arg Ser Thr Lys Gln Gln Gln Pro
111 645 650 655
112 Leu Val Ser Ile Leu Asp Phe Val Gly Phe
113 660 665
115 <210> SEQ ID NO: 2
116 <211> LENGTH: 2171
117 <212> TYPE: DNA
118 <213> ORGANISM: Macadamia integrifolia
120 <220> FEATURE:
121 <221> NAME/KEY: sig_peptide
122 <222> LOCATION: (1)...(85)
124 <221> NAME/KEY: mat_peptide
125 <222> LOCATION: (86)...(1999)
127 <400> SEQUENCE: 2
128 atggcgacaa atacatcaa tttatgttct cttcttttc tccctttact ctcccttttg
129 ttcacgacag ttgtcttttc tgaatgtgaa tttagcaggc aggaatatgt qgagtgcaaa 60
130 cqgcacalqca lqcaqtlqqa gacatcaqgc caqatucqtc qgtgttgtqaa tcaqtqcgat 120
131 aaqagatttq agatqgttct aqatgtatac accaaqaaqaa tccttcqaaq 180
132 gaatgcacaa acatggcagag gcatgtcaggc cagcaggaga gtggccccacg tcagcaacaa 240
133 tactgcacaa gacqctycaa gaaatataatgt..gaaagaagaag aagaataataa ccqacaacgt 300
134 gatccacacg agcaatacag gcaatgtcag aagcaatgtcc aacggccccc gacagagcc 360
135 cqtcacatqc aaacatgtca acaacgtgc qaqagqgat atqaaaqaa gaaacqtaaq 420
136 caaaaaaaa gatataaaga gcaacaacgt gaagacgaaag aaaaatgtaa agagcgaatg 480
137 aagaaagaag ataacaaaacg cgatccacaa caaaqagagt acgaaagactt ccqgaggcc 540
138 tycgacaaac aggayccacg tcaqcaqccac cagtgcacq taatgtccg agaqaqcc 600
139 agycaacacg gccgaggatgg cgatgtatgt aacccttcaga ggggaggccg cggcagatad 660
140 gagggaggag aagaggacg aagcgacaaac ccttactact tgcacaaacg aagcttaagt 720
141 acaagggtca ggaccaqqa agggccacate tcgttctgg agaacttcta tggtagatcc 780
142 aaqcttttac ycqcaactaa aaactatccq ttttgtqctcc tccgaggctaa ccccaaccc 840
143 ttctgtctcc ctaccactt yyatgcagat gcccattctt tggctatagg agggagaa 900
144 gcccccaaaa tcatccacca cgcacaaacaa gaatcttaca accttgcgtt tggqagacta 960
145 atcagaalcc cagetggaaac cacatcttac ttaatcaaaac gagacaacaa egagaggctc 1020
146 cacatagcca aqtttttaca gaccatatcc actcttggcc aatacaaggaa attttccca 1080
147 gctggaaqccc aaaacccaga gccgtaccc aqttttca gcaaaagagat ttcqagact 1140
148 ygcgtcaaca cacaacacaga gaatgtgcgt ygggtgttgg gacacaaagg ggaggggatlg 1200
149 ataattttgg cgtccacacg gcaatgtcgg gatgttgcic gagatgtcic agatgtcaaga 1260
150 cactggcata taaggatgg tggtaatca aecaggggac ttatcaatct qtcaacaaa 1320
151 aqggcactgt actccacaa atacqgtca gcttacgaa gtcggatgg tcaaaacctgaa 1380
152 caactccaaq acatgtcaat atcggttttc ataqccaaqg tcacccaaqg atccatgtq 1440
153 ggtcccttct tcaacacttgc gtcttacaaag gtggtagtgg tggctatgtq agagggcaqat 1500
154 qlggaaalgg calgcctca ctgttggaa agacacggcg gcccgggttgq aggaaaaagg 1560
155 catgaggagg aagaggatgt gcaatgtcgg cagtttgc gaaatgttgc gaagagqag 1620
156 gccatgttgc ttcgttgcagg tcatcccttc gtcttgcgtt tcatccggaa cggaaacttg 1680
157 ctgcatttttgc catttggaaat caatgcacaa aacaaccacg agaacttcc tgggggggaga 1740
158 gagagqaacg tgcttgcggca qatagagccaa caggcaatgg agcttagctt tggccgttcca 1800
159 aggaaagagg tggaaatggc attttttttttcc caggaccatgt ctatcttctt tccctggggccc 1860
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160 aggcacgacc agcaacagtc qccceqctcc accaaggcaac aacagcctct cgttccatt 1980
161 ctggaaattcg ttagtttcta aagtccaca aaaaagatgt tggttatgtat tataggtag 2040
162 taatctctaa ctcgggttat gaaqaqtgta aqaaqactaau aeqctaaatc cctaaqtaac 2100
163 taacctggcg agcttgcgtg tatgcaaata aagaqqaaca gtttccaac tttaaaaaaa 2160
164 aaaaaaaaaa a 2171
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 666
168 <212> TYPE: PRT
169 <213> ORGANISM: Macadamia integrifolia
171 <220> FEATURE:
172 <221> NAME/KEY: SIGNAL
173 <222> LOCATION: (1)...(28)
175 <221> NAME/KEY: PEPTIDE
176 <222> LOCATION: (29)...(666)
178 <400> SEQUENCE: 3
179 Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
180 1 5 10 15
181 Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
182 20 25 30
183 Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
184 35 40 45
185 Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
186 50 55 60
187 Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Asp Asp Pro Gln Thr
188 65 70 75 80
189 Asp Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro
190 85 90 95
191 Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu
192 100 105 110
193 Glu Gln Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Gln Tyr Glu Gln
194 115 120 125
195 Cys Gln Glu Arg Cys Gln Arg His Gln Thr G's Pro Arg His Met Gln
196 130 135 140
197 Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys
198 145 150 155 160
199 Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr
200 165 170 175
201 Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg
202 180 185 190
203 Glu Tyr Glu Asp Cys Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln
204 195 200 205
205 Gln Tyr Gln Cys Gln Arg Arg Cys Arg Glu Gln Gln Arg Gln His Gly
206 210 215 220
207 Arg Gly Gly Asp Leu Ile Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
208 225 230 235 240
209 Glu Glu Gly Glu Lys Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
210 245 250 255
211 Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
212 260 265 270

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213 Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
214      275          280          285
215 Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro
216      290          295          300
217 Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Thr Gly Gly Arg Gly
218      305          310          315          320
219 Ala Leu Lys Met Ile His Arg Asp Asn Arg Glu Ser Tyr Asn Leu Glu
220      325          330          335
221 Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
222      340          345          350
223 Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
224      355          360          365
225 Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
226      370          375          380
227 Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
228      385          390          395          400
229 Ala Leu Asn Thr Gln Ala Glu Arg Leu Arg Gly Val Leu Gly Gln Gln
230      405          410          415
231 Arg Glu Gly Val Ile Ile Ser Ala Ser Gln Glu Gln Ile Arg Glu Leu
232      420          425          430
233 Thr Arg Asp Asp Ser Glu Ser Arg Arg Trp His Ile Arg Arg Gly Gly
234      435          440          445
235 Gln Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
236      450          455          460
237 Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
238      465          470          475          480
239 Gln Leu Gln Asp Met Asp Val Ser Val Phe Ile Ala Asn Ile Thr Gln
240      485          490          495
241 Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
242      500          505          510
243 Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu
244      515          520          525
245 Ser Gly Arg His Gly Arg Arg Gly Gly Lys Arg His Glu Glu Glu
246      530          535          540
247 Glu Asp Val His Tyr Glu Gln Val Lys Ala Arg Leu Ser Lys Arg Glu
248      545          550          555          560
249 Ala Ile Val Val Pro Val Gly His Pro Val Val Phe Val Ser Ser Gly
250      565          570          575
251 Asn Glu Asn Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
252      580          585          590
253 His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
254      595          600          605
255 Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
256      610          615          620
257 Glu Glu Leu Phe Asn Ser Gln Asp Glu Ser Ile Phe Phe Pro Gly Pro
258      625          630          635          640
259 Arg Gln His Gln Gln Ser Ser Arg Ser Thr Lys Gln Gln Gln Pro
260      645          650          655
261 Leu Val Ser Ile Leu Asp Phe Val Gly Phe

```

PYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 12/28/2000
 PATENT APPLICATION: US/09/331,631A TIME: 08:00:59

Input Set : A:\CULLN23SEQ.txt
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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
 L:1238 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
 L:1238 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
 L:1238 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
 L:1240 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
 L:1240 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
 M:340 Repeated in SeqNo=31
 L:1253 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
 L:1253 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
 L:1253 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
 L:1255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
 L:1255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
 M:340 Repeated in SeqNo=32
 L:1268 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
 L:1268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
 L:1268 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
 L:1270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
 L:1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
 M:340 Repeated in SeqNo=33
 L:1284 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
 L:1284 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
 L:1284 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
 L:1286 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
 L:1286 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
 M:340 Repeated in SeqNo=34
 L:1300 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
 L:1300 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
 L:1300 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
 L:1302 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
 L:1302 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
 M:340 Repeated in SeqNo=35
 L:1316 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
 L:1316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
 L:1316 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
 L:1318 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
 L:1318 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
 M:340 Repeated in SeqNo=36
 L:1331 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:37
 L:1331 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:37
 L:1331 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:37
 L:1333 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:37
 L:1333 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:37
 M:340 Repeated in SeqNo=37
 L:1346 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
 L:1346 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
 L:1346 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38

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Input Set : A:\CULLN23SEQ.txt
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L:1348 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:1348 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
M:340 Repeated in SeqNo=38
L:1361 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:39
L:1361 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:39
L:1361 M:340 W: (46) "n" or "xad" used: Feature required, for SEQ ID#:39
L:1363 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:39
L:1363 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:39
M:340 repeated in SeqNo=39
L:1376 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:1376 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:1376 M:340 W: (46) "n" or "xad" used: Feature required, for SEQ ID#:40